

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Appl. No.	:	10/583,286
Cnfrm. No.	:	9818
Applicant(s)	:	Yoshio Yamauchi et al.
Filed	:	December 17, 2004
Title	:	METHOD FOR ANALYZING PROTEINS
TC/A.U.	:	none
Examiner	:	none
Docket No.	:	IWI-16646

Mail Stop PETITION  
Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

**PETITION UNDER RULE 1.182**

Sir:

In response to the Notification of Missing Requirements under 35 U.S.C. 371 mailed March 16, 2007, Applicants Petition the Commissioner under 37 C.F.R. 1.182 to accept the Declaration on file. The Notice states that the current Declaration does not comply with 37 C.F.R. 1.497(a) and (b) because it (1) fails to comply with either 37 C.F.R. 1.66 or 1.68, and (2) that the family name of the second inventor does not correspond with the name on the published application.

The second inventor's name was mistranslated from the Japanese language to the English language in the PCT application, published as WO 2005/059538 A1. The second inventor's name is, in fact,

**Takashi SHINKAWA**

As evidence of this, Applicants enclose copies of the following:

1. Copy of letter from Japanese Patent Attorney Yuji Iwahashi, the Japanese Patent Attorney in this patent application, which affirmatively states that "[t]he correct name of the second inventor is "Takashi SHINKAWA." Further, the letter states, in summary, that the Chinese characters used in Japanese writing corresponding to the family name of the second inventor may be translated as "SHINKAWA" or "ARAKAWA," and without context, it is impossible to determine which is intended.
2. Copy of the front page of the corresponding Canadian Patent Application, CA2550017 (A1), showing the name of the second inventor as "SHINKAWA, TAKASHI."

Based on the evidence presented, Applicants respectfully petition the Commissioner to accept the declaration executed on June 6, 2006, and filed together with the application on June 16, 2006 as sufficient to meet the requirements of 37 C.F.R. 1.497(a) and (b), as well as 37 C.F.R. 1.68.

The enclosed petition fee transmittal sheet (37 C.F.R. 1.17(f)) indicates that a petition fee of \$400 accompanies this petition. If there are any additional fees resulting from this communication, please charge the same to our Deposit Account No. 18-0160, our Order No. IWI-16646.

Respectfully submitted,

RANKIN, HILL, PORTER & CLARK LLP



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Enclosures

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October 13, 2006

via Facsimile & Air mail

RANKIN, HILL, PORTER & CLARK LLP  
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U.S.A.

**CONFIRMATION**

Re: U.S. Patent Application No. 10/583,286  
Your ref.: IWI-16646  
Our ref.: 058-13  
Title: METHOD FOR ANALYZING PROTEINS

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Dear Sir,

Thank you for your facsimile letter of March 26, 2007 with respect to the above-identified application.

We think that "the inventorship did not match as between the list of inventors specified in the International Application" means second inventors name  
"ARAKAWA / SHINKAWA".

**The correct name of the second inventor is "Takashi SHINKAWA".**

His name has not been record in the WIPO. It was not in the time at the stage of WIPO. So, there is no document of PCT/IB/306.

A Chinese character used in Japanese writing "新川" is reading "ARAKAWA" or "SHINKAWA" etc.. In Japan, about the name of a parson, the reading of Chinese Characters are various and it is not indicated in the certificate by a notary public.

Please take necessary procedure before due date.

Very truly yours,



for Yuji IWAHASHI

(12)

(21) 2 550 017

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(71)

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(54) PROCEDE D'ANALYSE DE PROTEINES

(54) PROTEIN ANALYSIS METHOD

(57)

It is intended to provide a protein analysis method whereby proteins can be identified and the quantification data can be obtained by a convenient procedure. Namely, a protein analysis method characterized by comprising: the step of cleaving two protein-containing samples individually with restriction enzymes at specific amino acid sites to give peptide chain-containing samples; the step of modifying peptide chains contained in the peptide chain-containing samples with labeling compounds having different masses due to isotopes so as to impart different masses to the peptide chains; the step of mixing the isotope-labeled peptide chain-containing samples and fractionally quantifying the sample mixture for individual peptide chains so as to determine a content ratio; the step of selecting peptide chains to be subjected to amino acid sequence identification from the peptide chains and identifying the amino acid sequences of the peptide chains; the step of specifying proteins corresponding to the peptide chains; and the step of determining the content ratio of the thus specified proteins based on the fractional quantification data of the peptide chains.

